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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=2; day=5; hr=14; min=17; sec=45; ms=80;]

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Reviewer Comments:

<210> 7

<211> 54

<212> DNA

<213> Oligonucleotide Primer CF59

<400> 7

cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc 54

The above <213> response is invalid, also similar responses were found in sequence id#'s 10 and 11. FYI, these responses can be inserted into section <220> to <223>.

Application No: 10584438 Version No: 1.0

Input Set:**Output Set:**

Started: 2008-01-29 15:17:14.169
Finished: 2008-01-29 15:17:15.923
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 754 ms
Total Warnings: 20
Total Errors: 1
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)

Input Set:

Output Set:

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Total Warnings: 20
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No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

<210> 1
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Linker VC053

 <400> 1
 gatctttgga taagagagac gctcacaagt ccgaagtcgc tcaccggt 48

 <210> 2
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Linker VC054

 <400> 2
 ccttgaaccg gtgagcgact tcggacttgt gagcgtctct cttatccaaa 50

 <210> 3
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Linker VC055

 <400> 3
 gatctttgga taagagagac gctcacaagt ccgaagtcgc tcatcgat 48

 <210> 4
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Linker VC056

 <400> 4
 ccttgaatcg atgagcgact tcggacttgt gagcgtctct cttatccaaa 50

 <210> 5
 <211> 86
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Oligonucleotide Linker VC057

 <400> 5
 tcaaggacct aggtgaggaa aacttcaagg ctttggtctt gatcgctttc gctcaatact 60
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 <210> 6

<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Linker VC058

<400> 6
gtgatcttcg aatggacatt gttgcaagta ttgagcgaaa gcgatcaaga ccaaagcctt 60
gaagttttcc tcacctaggt 80

<210> 7
<211> 54
<212> DNA
<213> Oligonucleotide Primer CF59

<400> 7
cgatagatct ttggataaga gagggccacc acctggcccc cctcgagttt cccc 54

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide linker SEQ ID 8

<400> 8
Gly Gly Gly Gly Ser
1 5

<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide linker SEQ ID 9

<400> 9
Gly Gly Gly Ser
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<210> 10
<211> 17
<212> PRT
<213> Stanniocalcin signal peptide sequence

<400> 10
Met Leu Gln Asn Ser Ala Val Leu Leu Leu Val Ile Ser Ala Ser
1 5 10 15

Ala

<210> 11
<211> 22

<212> PRT
<213> Consensus signal sequence

<400> 11
Met Pro Thr Trp Ala Trp Trp Leu Phe Leu Val Leu Leu Leu Ala Leu
1 5 10 15

Trp Ala Pro Ala Arg Gly
20

<210> 12
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer CF60

<400> 12
ggccatcgat gagcgacttc ggacttgtga gcgtccagcc gagtcttcag cagcagcagt 60
cccttc 66

<210> 13
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer CF61

<400> 13
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<210> 14
<211> 45
<212> DNA
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<220>
<223> Oligonucleotide Primer CF62

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<210> 15
<211> 2358
<212> DNA
<213> Artificial Sequence

<220>
<223> N-terminal IL11-albumin fusion

<400> 15
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ctggacagca cgtgctcct gacctgctct ctctggcgg acacgcggca gctggctgca 180
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caagctgctt tgggtttg 2358

```

<210> 16

<211> 786

<212> PRT

<213> Artificial Sequence

<220>

<223> N-terminal IL11-albumin fusion

<400> 16

Met Lys Trp Val Phe Ile Val Ser Ile Leu Phe Leu Phe Ser Ser Ala

1 5 10 15

Tyr Ser Arg Ser Leu Asp Lys Arg Gly Pro Pro Pro Gly Pro Pro Arg

20 25 30

Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser Thr Val Leu Leu Thr

35 40 45

Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala Ala Gln Leu Arg Asp

50 55 60

Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp Ser Leu Pro Thr Leu
 65 70 75 80

Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln Leu Pro Gly Val Leu
 85 90 95

Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu Arg His Val Gln Trp
 100 105 110

Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr Leu Glu Pro Glu Leu
 115 120 125

Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu Arg Arg Leu Gln Leu
 130 135 140

Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro Pro Asp Pro Pro Ala
 145 150 155 160

Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly Gly Ile Arg Ala Ala
 165 170 175

His Ala Ile Leu Gly Gly Leu His Leu Thr Leu Asp Trp Ala Val Arg
 180 185 190

Gly Leu Leu Leu Leu Lys Thr Arg Leu Asp Ala His Lys Ser Glu Val
 195 200 205

Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val
 210 215 220

Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro Phe Glu Asp His
 225 230 235 240

Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys Thr Cys Val Ala
 245 250 255

Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His Thr Leu Phe Gly
 260 265 270

Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr Tyr Gly Glu Met
 275 280 285

Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn Glu Cys Phe Leu
 290 295 300

Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu Val Arg Pro Glu
 305 310 315 320

Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu Glu Thr Phe Leu
 325 330 335

Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro Tyr Phe Tyr Ala
 340 345 350

Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala Ala Phe Thr Glu
 355 360 365

Cys	Cys	Gln	Ala	Ala	Asp	Lys	Ala	Ala	Cys	Leu	Leu	Pro	Lys	Leu	Asp	370	375	380	
Glu	Leu	Arg	Asp	Glu	Gly	Lys	Ala	Ser	Ser	Ala	Lys	Gln	Arg	Leu	Lys	385	390	395	400
Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	Glu	Arg	Ala	Phe	Lys	Ala	Trp	Ala	405	410	415	
Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	Pro	Lys	Ala	Glu	Phe	Ala	Glu	Val	420	425	430	
Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	Lys	Val	His	Thr	Glu	Cys	Cys	His	435	440	445	
Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	Asp	Arg	Ala	Asp	Leu	Ala	Lys	Tyr	450	455	460	
Ile	Cys	Glu	Asn	Gln	Asp	Ser	Ile	Ser	Ser	Lys	Leu	Lys	Glu	Cys	Cys	465	470	475	480
Glu	Lys	Pro	Leu	Leu	Glu	Lys	Ser	His	Cys	Ile	Ala	Glu	Val	Glu	Asn	485	490	495	
Asp	Glu	Met	Pro	Ala	Asp	Leu	Pro	Ser	Leu	Ala	Ala	Asp	Phe	Val	Glu	500	505	510	
Ser	Lys	Asp	Val	Cys	Lys	Asn	Tyr	Ala	Glu	Ala	Lys	Asp	Val	Phe	Leu	515	520	525	
Gly	Met	Phe	Leu	Tyr	Glu	Tyr	Ala	Arg	Arg	His	Pro	Asp	Tyr	Ser	Val	530	535	540	
Val	Leu	Leu	Leu	Arg	Leu	Ala	Lys	Thr	Tyr	Glu	Thr	Thr	Leu	Glu	Lys	545	550	555	560
Cys	Cys	Ala	Ala	Ala	Asp	Pro	His	Glu	Cys	Tyr	Ala	Lys	Val	Phe	Asp	565	570	575	
Glu	Phe	Lys	Pro	Leu	Val	Glu	Glu	Pro	Gln	Asn	Leu	Ile	Lys	Gln	Asn	580	585	590	
Cys	Glu	Leu	Phe	Glu	Gln	Leu	Gly	Glu	Tyr	Lys	Phe	Gln	Asn	Ala	Leu	595	600	605	
Leu	Val	Arg	Tyr	Thr	Lys	Lys	Val	Pro	Gln	Val	Ser	Thr	Pro	Thr	Leu	610	615	620	
Val	Glu	Val	Ser	Arg	Asn	Leu	Gly	Lys	Val	Gly	Ser	Lys	Cys	Cys	Lys	625	630	635	640
His	Pro	Glu	Ala	Lys	Arg	Met	Pro	Cys	Ala	Glu	Asp	Tyr	Leu	Ser	Val	645	650	655	
Val	Leu	Asn	Gln	Leu	Cys	Val	Leu	His	Glu	Lys	Thr	Pro	Val	Ser	Asp	660	665	670	

Arg Val Thr Lys Cys Cys Thr Glu Ser Leu Val Asn Arg Arg Pro Cys
 675 680 685

Phe Ser Ala Leu Glu Val Asp Glu Thr Tyr Val Pro Lys Glu Phe Asn
 690 695 700

Ala Glu Thr Phe Thr Phe His Ala Asp Ile Cys Thr Leu Ser Glu Lys
 705 710 715 720

Glu Arg Gln Ile Lys Lys Gln Thr Ala Leu Val Glu Leu Val Lys His
 725 730 735

Lys Pro Lys Ala Thr Lys Glu Gln Leu Lys Ala Val Met Asp Asp Phe
 740 745 750

Ala Ala Phe Val Glu Lys Cys Cys Lys Ala Asp Asp Lys Glu Thr Cys
 755 760 765

Phe Ala Glu Glu Gly Lys Lys Leu Val Ala Ala Ser Gln Ala Ala Leu
 770 775 780

Gly Leu
 785

<210> 17
 <211> 762
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mature N-terminal IL11-albumin fusion

<400> 17
 Gly Pro Pro Pro Gly Pro Pro Arg Val Ser Pro Asp Pro Arg Ala Glu
 1 5 10 15

Leu Asp Ser Thr Val Leu Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg
 20 25 30

Gln Leu Ala Ala Gln Leu Arg Asp Lys Phe Pro Ala Asp Gly Asp His
 35 40 45

Asn Leu Asp Ser Leu Pro Thr Leu Ala Met Ser Ala Gly Ala Leu Gly
 50 55 60

Ala Leu Gln Leu Pro Gly Val Leu Thr Arg Leu Arg Ala Asp Leu Leu
 65 70 75 80

Ser Tyr Leu Arg His Val Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser
 85 90 95

Leu Lys Thr Leu Glu Pro Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp
 100 105 110

Arg Leu Leu Arg Arg Leu Gln Leu Leu Met Ser Arg Leu Ala Leu Pro
 115 120 125

Gln	Pro	Pro	Pro	Asp	Pro	Pro	Ala	Pro	Pro	Leu	Ala	Pro	Pro	Ser	Ser	130	135	140	
Ala	Trp	Gly	Gly	Ile	Arg	Ala	Ala	His	Ala	Ile	Leu	Gly	Gly	Leu	His	145	150	155	160
Leu	Thr	Leu	Asp	Trp	Ala	Val	Arg	Gly	Leu	Leu	Leu	Leu	Lys	Thr	Arg	165	170	175	
Leu	Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	180	185	190	
Glu	Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	195	200	205	
Gln	Gln	Cys	Pro	Phe	Glu	Asp	His	Val	Lys	Leu	Val	Asn	Glu	Val	Thr	210	215	220	
Glu	Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	225	230	235	240
Lys	Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	245	250	255	
Leu	Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	260	265	270	
Pro	Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln	His	Lys	Asp	Asp	Asn	Pro	Asn	275	280	285	
Leu	Pro	Arg	Leu	Val	Arg	Pro	Glu	Val	Asp	Val	Met	Cys	Thr	Ala	Phe	290	295	300	
His	Asp	Asn	Glu	Glu	Thr	Phe	Leu	Lys	Lys	Tyr	Leu	Tyr	Glu	Ile	Ala	305	310	315	320
Arg	Arg	His	Pro	Tyr	Phe	Tyr	Ala	Pro	Glu	Leu	Leu	Phe	Phe	Ala	Lys	325	330	335	
Arg	Tyr	Lys	Ala	Ala	Phe	Thr	Glu	Cys	Cys	Gln	Ala	Ala	Asp	Lys	Ala	340	345	350	
Ala	Cys	Leu	Leu	Pro	Lys	Leu	Asp	Glu	Leu	Arg	Asp	Glu	Gly	Lys	Ala	355	360	365	
Ser	Ser	Ala	Lys	Gln	Arg	Leu	Lys	Cys	Ala	Ser	Leu	Gln	Lys	Phe	Gly	370	375	380	
Glu	Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val	Ala	Arg	Leu	Ser	Gln	Arg	Phe	385	390	395	400
Pro	Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser	Lys	Leu	Val	Thr	Asp	Leu	Thr	405	410	415	
Lys	Val	His	Thr	Glu	Cys	Cys	His	Gly	Asp	Leu	Leu	Glu	Cys	Ala	Asp	420	425	430	

Asp Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile
435 440 445

Ser Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser
450 455 460

His Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro
465 470 475 480

Ser Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr
485 490 495

Ala Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala
500 505 510

Arg Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys
515 520 525

Thr Tyr Glu Thr Thr Leu Glu Lys Cys